

GenCore version 5.1.6
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OM protein - nucleic search, using frame-plus.p2n model

Run on: May 30, 2003, 04:18:46 ; Search time 3433 Seconds
(without alignments) 3433.334 Million cell updates/sec

Title: US-09-934-900-2
Perfect score: 2150
Sequence: 1 MLSTLFEKFEVYNNRHVIKTM.....KMKKHGKVFMSIFNKELL 405

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2.1/USFO/spool/US09934900/runat_23052003.160451.15193/app.query.fasta.1.583
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-ONITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
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-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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2: gb_htg:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2150	100.0	1560	6	AX392312 Sequence
2	1661	77.3	1717	6	AX367139 Sequence
3	1646	76.6	1470	8	AF139377 Lupinus l
4	1466	68.2	1395	8	AY085086 Arabidops
5	1394	64.8	1284	8	AS060377
6	1338.5	62.3	1415	6	AX392322 Sequence
7	1337	62.2	1337	6	TAU07597 Thunbergia
8	1322.5	61.5	1318	6	AX392326 Sequence
9	1317	61.3	1576	8	SNM5CPD
10	1313	61.1	1443	8	TAU07605
11	1306	60.7	1507	8	POTSACPD
12	1301	60.5	1651	8	AY087294
13	1300	60.5	1243	6	I13990
14	1299	60.4	1643	8	RCCSACPD
15	1298	60.4	1279	8	AY128883
16	1298	60.4	1583	8	AY099784 Arabidops
17	1296.5	60.3	1407	8	CUS5ACPD
18	1295.5	60.3	1768	8	SCSACPD
19	1295	60.2	1662	8	RCSSTA
20	1295	60.2	1668	6	I90191
21	1292	60.1	1319	8	TAU07552
22	1291	60.0	1200	8	AF315600
23	1288	59.9	13192	8	AC006423
24	1283	59.7	1533	6	I16556
25	1283	59.7	1533	6	I19664
26	1283	59.7	1533	6	I90189
27	1283	59.7	1533	8	CAH5ACPD
28	1279	59.5	1610	8	SONACPD
29	1278.5	59.5	1335	8	HAU91339
30	1278	59.4	1580	8	SSMSACPD
31	1276.5	59.4	1623	8	SOVSACPD
32	1271.5	59.1	168033	2	AP003405
33	1271.5	59.1	200183	8	AP003227
34	1270	59.1	1493	8	OEU58141
35	1268.5	59.0	1426	8	HAU91340
36	1266	58.9	1517	8	AF116861
37	1266	58.9	1524	6	A74273
38	1266	58.9	1524	6	BNSACPD
39	1265.5	58.9	1715	8	EGU68756
40	1263	58.7	1495	6	I90194
41	1263	58.7	1495	8	BR5ACP
42	1263	58.7	1495	8	BNACPD
43	1260	58.6	1548	8	AF172728
44	1259	58.6	1567	8	AY088096
45	1258.5	58.5	1206	8	AF395441

RESULT 1

ALIGNMENTS

AX392312 1560 bp DNA linear PAT 23-MAR-2002
 LOCUS AX392312
 DEFINITION Sequence 1 from Patent WO0216565.
 ACCSSION AX392312
 VERSION AX392312.1 GI:19700680
 KEYWORDS
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 REFERENCE 1
 AUTHORS Booth, J.R., Cahoon, R.E., Hitz, W.D., Kinney, A.J. and Yadav, N.S.
 TITLE Nucleotide sequences of a new class of diverged delta-9
 steroyl-acp desaturase genes
 JOURNAL Patent: WO 0216565-A 1 28-FEB-2002.
 FEATURES
 source E. I. du Pont de Nemours and Company (US)
 location/Qualifiers
 1. 1560
 /organism="Glycine max"
 /db_xref="taxon:3847"
 BASE COUNT 402 a 360 c 443 g 355 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 7.59e-167 Length: 1560
 Score: 2150.00 Matches: 405
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
 US-09-934-900-2 (1-405) x AX392312 (1-1560)

DB 647 GAGGAAAACAGACACGGGAGTCTCAGAACTATTGTATCTCTCGGAGGCTTAC 706
 QY 201 MetalaValaGluValThrValHisValLeuIleSerAlaGlyMetAspProGlyThr 220
 DB 707 ATGGCTAAGTGTGAAAAGACCGGTACATTACCTATTTCAGTGGCATGGACCTGGGACA 766
 QY 221 AspAsnAsnProTyrLeuGlyPheValTyrThrSerPheGlnGluArgAlaThrPheVal 240
 DB 767 GACAAACACCCATATTGTGGGTTGTGTACAGTCATTCACAGAGGACCAACATTTGTG 826
 QY 241 AlaHisGlyAsnThrAlaArgLeuAlaValGlyGlyValAspProValLeuAlaArgLeu 260
 DB 827 GCGCACGGGACACGGCTCGGCTCGGAGAGGGGGGAGATCCAGTGTGGCGGCTTA 886
 QY 261 CysGlyThrIleAlaAlaAspGluValArgHisGlnAlaValTyrSerArgIleValGlu 280
 DB 887 TCGGGACCATTCGACCGGACGAGAGCGGACGAGAACCGGTACTCAAGATTCGGGAG 946
 QY 281 LysLeuLeuGluValAspProThrGlyAlaMetValAlaIleGlyAsnMetMetGlyLys 300
 DB 947 AAGCTTCTGGAAGTGGACCCACCGGGCCAAATGTGTCATAGGAAATGATGGAGAAG 1006
 QY 301 LysIleThrMetProAlaHisLeuMetTyrAspGlyAspAspProArgLeuPheGlnHis 320
 DB 1007 AAGATTCAGATGCGGCGACCTTATGTACGATGGAGATGATCCAGGCTATTCCAGCAC 1066
 QY 321 TyrSerAlaValAlaGlnArgIleGlyValTyrThrAlaAsnAspTyrAlaAspIleLeu 340
 DB 1067 TACTCGCGCTGTGGCGGACGAGCATAGGCGTGTACACCGCAACAGACTACGACATCTTG 1126
 QY 341 GluPheLeuValGluArgTyrPheArgLeuGluLysLeuGlyLysLeuMetAlaGluLys 360
 DB 1127 GAGTTCTCGTTCAGACGCTGAGATGTGAGAAAGCTTGAAGCATTTGATGCTGAGGGGAG 1186
 QY 361 ArgAlaGlnAspPheValGlyGlyLeuAlaProArgIleArgArgLeuGlnGluArgAla 380
 DB 1187 CCGGCGCAGAGATTCTGTGTGGTGGCGGCGGAGGATTAGAGGTTGCAAGACCGGCT 1246
 QY 381 AspGluArgAlaArgLysMetLysLysHisGlyValLysPheSerTrpIlePheAsn 400
 DB 1247 GATGACGAGCGCGTGAAGTGAAGAAAGCATCATGGCGTTAAGTTCAGTTGATTTTCAT 1306
 QY 401 LysGluLeuLeuLeu 405
 DB 1307 AAAAATTCCTTTTG 1321
 RESULT 2
 LOCUS AX367139 1717 bp DNA linear PAT 16-FEB-2002
 DEFINITION Sequence 24 from Patent WO020904.
 ACCSSION AX367139
 VERSION AX367139.1 GI:1885340
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Glasman, K.F., Gordon-Kamm, W.J., Kinney, A.J., Lowe, K., Stecca, K.L.
 and Nichols, S.E.
 TITLE Recombinant constructs and their use in reducing gene expression
 JOURNAL Patent: WO 020904-A 24 03-JAN-2002;
 E. I. du Pont de Nemours and Company (US); PIONEER HI-BRED
 INTERNATIONAL, INC. (US)
 FEATURES
 source 1. 1717
 location/Qualifiers
 1. 1717
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="ELVISLIVES complementary region of pBS68"
 BASE COUNT 399 a 430 c 478 g 410 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 9.29e-127 Length: 1717

Score:	1661.00	Matches:	331
Percent Similarity:	95.95%	Conservative:	1
Best Local Similarity:	95.66%	Mismatches:	10
Query Match:	77.26%	Indels:	6
DB:	6	Gaps:	1

US-09-934-900-2 (1-405) x AX367139 (1-1717)

[illegible][illegible]

RESULT 3
AF139377

AF139377

LOCUS	AF139377	1470 bp	mRNA	linear	PLN 17-MAR-2000
DEFINITION	Lupinus luteus stearyl acyl carrier protein desaturase L1dd3A20				

ACCESSION	VERSION	AF139377.1	GI:4704823	AF139377	mRNA, complete cds.

KEYWORDS	AF133577.1	GI:4704625
VERSION		
SOURCE		
	Lupinus luteus.	

ORGANISM
Lupinus luteus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae;

Lupinus.
1 (bases 1 to 1470)

TITLE Identification of new nodulin cDNAs from yellow lupine by differential display

JOURNAL
REFERENCE
2 (bases 1 to 1470)
Plant Sci. 151 (1), 75-83 (2000)
differential display

ANNOUNCED
 2 (pages 1 to 140)
 AUTHORS Swiderski, M. R., Zaborowska, Z. and Legocki, A. B.
 TITLE Direct Submission

JOURNAL Submitted (30-MAR-1999) Biology, Indiana University, Jordan Hall
142, Bloomington 47405, USA

FEATURES	Location/Qualifiers
source	1. .1470

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/organism="Lupinus luteus"
/cultivar="Ventus"
/ab_vrof="Favon, 1973"

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/cooim_stear1-1
/product="stearoyl acyl carrier protein desaturase
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protein_id="AAD28287.1"
/db_xref="GI:4704824"

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EKNOWNGDRTVEGDSBUTRACOGSTLYLGGSDMUNATUWZTADPDRSAL

FVSHGNTARLAKNEGDPYLARTCGTIADEKXHNENASRIVEKLELLEDPGTGAWAIG
YMMOKITMPAHLMYDGEDPKLFEDHFSVAQRGVYTNADYADGLEFLIGRWLEKVO
YDEKXZADDEUCIADDPKLOBBADAPKAPKAPVAVGEGENZETI#

BASE COUNT	431 a	304 c	352 g	383 t
ORIGIN	LNDGKKAQDFVCGLAPRIIRLQDERAEKARKKKPHAVKFSWLNKELL"			

Alignment Scores:

Assignment Codes:	1.29e-125	Length:	1470
Pred. No.:		Matches:	311
Score:	1646.00		

Percent Similarity:	90.00%	Conservative:	40
Best Local Similarity:	79.74%	Mismatches:	33

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Query Match: 76.56% Index: 6
DB: 8 Gaps: 5
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US-09-934-900-2 (1-405) x AF139377 (1-1470)

18 Lys^{Thr}Met^{Gln}Ile^{Arg}Thr^{Cys}His^{Ser}Ile^{Thr}Thr^{Gln}Ile^{Thr}Leu^{Pro}Gln^{Leu}Pro 37

Db 109 AAAAAATCGAGATTCAACCTGCTACTATCAGAAATCAAAATCTTCT---CTTCA 165

Oy 38 CysSerSerArgLysAlaHisHisLeuProLeuAsnAlaValSer 57
::: ||| ::|||::: |||::: |||

Db 166 TGGCCAGAAGAACTGGCCGCCACAAA---ATGCTGCCACCCATA---GCAGCCATCTCC 219

58 Alalapro-----PheylsAlaArgylsAlahlsSsetmetProciulslslyslsGlu 75

DB 220 GCCACACCGCGTGGCTGAATCTCCTAAGACCCACTCATGCCCACAGAAAAGATAGAG 2/9

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QY 76 IlePheLysSerLeuGluGlyTTPAlaSerGluTTPValLeuProLeuLeuLysProVal 95
Db 280 ATATTCAGTCACTTGAGAGCTGGCATCAACATCGGTCTTCCACTTGTGAAGCCAGTGC 339
QY 96 GluGlnCysTrpGlnProGlnAsnPheLeuProAspProSerLeuProHisGluGluPhe 115
Db 340 GAACAAATGCTGGACGCCAAGAAATTCCTCCCTGACCCCTCTTGGCGTTGGGGAATTC 399
QY 116 SerHisGlnValLysGluLeuArgGluArgGluThrLysGluLeuProAspGluTyrPheVal 135
Db 400 ACGGATCAGCTGAAGGCCCTCCCTGACCCGACGCGGAGAGTCCGCGAGGAGTACTTCTG 459
QY 136 ValLeuValGlyAspMetValThrGluAspAlaLeuProThrTyrGlnThrMetLeuAsn 155
Db 460 GTATTGGTGGTACATGATACAGAGAGATCGCTGCCAAGATACAGATGATGATCAAC 519
QY 156 AsnLeuAspGlyValLysAspAspSerGlyThrSerProSerProThrAlaValTTPThr 175
Db 520 AATCTTGATGGGTAAAGGATGAGACTGGGTCAAGCCGACGCCATGGCTTATATGACC 579
QY 176 ArgAlaThrPheAlaGluGluAsnArgHisGlyAspLeuLeuArgThrTyrLeuTyrLeu 195
Db 580 CCGGCTTGACCTGCAGAAAGAAAAGACATGAGATTTGCTTGAACCTTATTTGTATCTT 639
QY 196 SerGlyArgValAspMetAlaLysValGluLysThrValHisTyrLeuLeuSerAlaGly 215
Db 640 TCTGCTGCTGTGATATGAGAAAGATGAGAAAGATGCTGTACATGATTTATGATCGGC 699
QY 216 MetAspProGlyThrAspAsnAsnProTyrLeuGluGlyPheValTyrThrSerPheGlnGlu 235
Db 700 ATGAGCCCGGGAACAGAAACCAACCCATATTTGGATTTGTATACAGCTATATCCAGAG 759
QY 236 ArgAlaThrPheValAlaHisGlyAsnThrAlaArgLeuAlaLysGluGlyAspPro 255
Db 760 CGAGCCCATTTGCTGCATGCGCAACACACAGCTCGGTACCCAAAGAGGTGGCGATCCA 819
QY 256 ValLeuAlaArgLeuGlyGlyThrThrLeaAlaAspGluLysArgHisGluAsnAlaTyr 275
Db 820 GTCTGCTGCTGCATATGCGGACCATTTGCTGCAGACAGAAAGCCGACGAGAAATGCCTAT 879
QY 276 SerArgIleValGluLysLeuLeuGluValAspProThrGlyAlaMetValAlaIleGly 295
Db 880 TCCAGATTCGTCGAGAAAGCTTCTAGAAATTCGACCCCAAGACCAATAGGTAGCTATTTGGA 939
QY 296 AsnMetMetGluLysLysIleThrMetProAlaHisLeuMetTyrAspGlyAspAspPro 315
Db 940 GACATGATGCGAAGAAAAGATCACATGCCACACACTTGATGTACATGAGAGAAGACCTT 999
QY 316 ArgLeuPheGluHisTyrSerAlaValAlaGlnArgIleGlyValTyrThrAlaAsnAsp 335
Db 1000 AACTTGTTCGATCACTCTCTCGCGGCGGCGACGAAATGGGTTCACAGGCCAATGAT 1059
QY 336 TyrAlaAspIleLeuGluPheLeuValGluArgTyrArgLeuGluLysLeuGluGluLeu 355
Db 1060 TATGCGATATATCTTGGATTTGATCGAGCGGTGGAGATTTGGAAGAGTTCAAGATTTG 1119
QY 356 MetAlaGluGlyLysArgAlaGlnAspPheValCysGlyLeuAlaProArgIleArgArg 375
Db 1120 AAGAGTAGGAGGAAGAAGACACAGATTTGTGTGTGGTGGCAGCGAGATCAGAGAG 1179
QY 376 LeuGlnGluArgAlaAspGluArgAlaArgLysMetLysLysHisGlyValLysPhe 395
Db 1180 TTTCAGAGAGCTGCTGATGAAAGAGCGCGCAAAATGAACCG--CATGCTGTGAATTC 1236
QY 396 SerTrpIlePheAsnLysGluLeuLeuLeu 405
Db 1237 AGCTGGAATTTTATATAAGAGATTATTTTG 1266

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RESULT 4
 LOCUS AY085086 1395 bp mRNA linear PLN 21-JUN-2002
 DEFINITION Arabidopsis thaliana clone 12736 mRNA, complete sequence.

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ACCESSION AY085086
VERSION AY085086.1 GI:21403796
KEYWORDS FLI CDNA.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1395)
Haas, B.J., Volkovskiy, N., Town, C.D., Troukhan, M., Alexandrov, N.,
Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
Genome Biol. (2002) In press
2 (bases 1 to 1395)
Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
Feldmann, K.
Full-length cDNA from Arabidopsis thaliana
Unpublished
3 (bases 1 to 1395)
Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
Feldmann, K.
Direct Submission
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to RIGR and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent of
the clones are estimated to be 5'-truncated; less than one percent
are 3'-truncated; approximately two percent represent alternative
splice variants, including unspliced introns and spliced exons; one
percent may contain premature stop codons; five percent may have
frame shifts in a coding region. A sequence is considered to be
5'-truncated if it lacks the translation initiation start (ATG). A
sequence is considered to be 3'-truncated if it lacks the
C-terminal end of the encoded protein. Please note that these cDNA
sequences are derived from the WS or Uler ecotypes and therefore
may contain polymorphisms when compared to sequences from Col-0.
GenSet carried out the library production and sequencing of the
full-length clones. Ceres, Inc. carried out the clustering of the
5' sequences, selection of clones, and sequence assembly.
FEATURES
source
location/Qualifiers
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/clone="12758"
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BASE COUNT 352 a 331 c 342 g 370 t
ORIGIN
Alignment Scores:
Pred. No.: 1395
Score: 1466.00
Length: 282
Percent Similarity: 82.35% Conservative: 40
Best Local Similarity: 72.12% Mismatches: 63
Query Match: 68.19% Indels: 6
DB: 8 Gaps: 2

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US-09-934-900-2 (1-405) x AY085086 (1-1395)
 QY 18 LysThrMetClnIleArgThrCysHisSerIleThrThrGlnThrLeuProGlnLeuPro 37

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Db      45 AAAATGCTTACGACAAAGTCTTCTCTCTCCACCAACCAATGGGTACATAATGCA 104
Oy      38 CysSerSerArgLysAlaHisHisArgHisLeuProProLeuAsnAlaValSer 57
Db      105 TCTCCGCTCTACTTTTCTCGCTCTGCCCCCGGTGAGCGCAAGATATGCGCGTGC 161
Oy      58 AlaAlaProPheLys-----AlaArgLysAlaHisSerMetProProGlu 72
Db      162 GCACACCTGTGAGCGCGCTCTAAACCAACCAAAACAAATCCACACCATCCACCGAG 221
Oy      73 LysLysGluLeuPheLysSerLeuGluGlyTrpAlaSerGluTrpValLeuProLeu 92
Db      222 AAAATGAGATATTCAAATCTTTAGATGATGGCCACGATCAATCTTCCTCTCTC 281
Oy      93 LysProValGluGlnCysTrpGlnProGlnAsnPheLeuProAspProSerLeuProHis 112
Db      282 AAACCCGTGACCAATGTGGCAACCGCTTCTTTACCCGACCGCGCTTACCCCTTC 341
Oy      113 GluGluPheSerHisGlnValLysGluLeuArgGluArgTrpLysGluLeuProAspGlu 132
Db      342 TCCAGATTACCGACGACGAGTCTGTGAGCTGAGGGAAGAAATGCGCTCCTCCAGACGA 401
Oy      133 TyrPheValValLeuValGlyAspMetValThrGluAspAlaLeuProThrTyrGlnThr 152
Db      402 TACTTCGTGTGTGTGTGTGAGATATGATTAACGAGGAGCGGCTTGCCTACTTACACAGC 461
Oy      153 MetLeuAsnLeuAspGlyValLysAspAspSerGlyThrSerProSerProTrpAla 172
Db      462 ATGTATCAACACCTTGACGGCGTGAAGGACGACAGCTGTGCAAGTGAAGACGCGCTGCA 521
Oy      173 ValTrpThrArgAlaTrpThrAlaGluGlnAsnArgHisGlyAspLeuLeuArgThrTyr 192
Db      522 AGTTGGACAAACGCTGACGCGCTGAAGAGATGCTCATGTGATTTGTCGGGCTTAC 581
Oy      193 LeuTyrLeuSerGlyArgValAspMetAlaLysValGluLysThrValHisTyrLeuIle 212
Db      582 TTGTACTATATCGGCGGTGTGATGATGCTTATGTGTGAACGACCGCTTACACATCTCATC 641
Oy      213 SerAlaGlyMetAspProGlyThrAspAsnAsnProTyrLeuGlyPheValTyrThrSer 232
Db      642 GGCTCGGGCATGATCTCCAGAACTGAGAACATCATCTAGGTTTCTGTACACGCTCA 701
Oy      233 PheGlnGluArgAlaThrPheValAlaHisGlyAsnThrAlaArgLeuAlaLysGluLys 252
Db      702 TTCCAAAGACGACGACATTTGTGTCTACGCAACACGCGCATGACCAAGCGCGCA 761
Oy      253 GlyAspProValLeuAlaArgLeuGlyGlyThrIleAlaAlaAspGluLysArgHisGlu 272
Db      762 GGAGATCCTGTCTCGCTCGAATCTGCGGACCAATTCGACGTGACGAGAACGCCCATGA 821
Oy      273 AsnAlaTyrSerArgIleValGluLysLeuGluGluValAspProThrGlyAlaMetVal 292
Db      822 AACCTTACGATGATCTGTGAGAAAGCTCTCGAGATCGACCTTAACGCGTACGTCCA 881
Oy      293 AlaIleGlyAsnMetMetGluLysLysIleThrMetProAlaHisLeuMetTyrAspGly 312
Db      882 GCCGTGGCGGACATGATCGGAAAGATCAATTCGCGCTCATTTATGACAGACGCT 941
Oy      313 AspAspProArgLeuPheGluHisTyrSerAlaValAlaGlnArgIleGlyValTyrThr 332
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Oy      353 GluGlyLeuMetAlaGluGlyLysArgAlaGlnAspPheValCysGlyLeuAlaProArg 372
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Oy      21 GlnIleArgThrCysHisSerIleThrThrGlnIleuProGlnIleuProCysSerSer 40

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RESULT 6
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LOCUS AX392322 1415 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 11 from Patent WO0216565.
ACCESSION AX392322
VERSION AX392322.1 GI:19700685
KEYWORDS
SOURCE
ORGANISM
Zea mays.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 Booth, J.R., Cahoon, R.E., Hitz, W.D., Kinney, A.J. and Yadav, N.S.
Nucleotide sequences of a new class of diverged delta-9
stearoyl-acyl desaturase genes
Patent: WO 0216565-A 11 28-FEB-2002;
E. I. du Pont de Nemours and Company (US)

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ACCESSION U07597
VERSION U07597.1 GI:533083
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1 (bases 1 to 1337)
AUTHORS Cahoon,E.B., Becker,C.K., Shanklin,J. and Ohlroge,J.B.
TITLE cdnas for isoforms of the delta 9-stearyl-acyl carrier protein
JOURNAL Plant Physiol. 106 (2), 807-808 (1994)
MEDLINE 95083771
PUBMED 7991701
REFERENCE 2 (bases 1 to 1337)
AUTHORS Cahoon,E.B.

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TITLE Direct Submission
JOURNAL Submitted (08-MAR-1994) Cahoon E. B., Brookhaven National
Laboratory, Biology, Upton, NY 11973, USA
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 KEYWORDS
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhacoidae; Oryzeae; Oryza.
 REFERENCE
 AUTHORS Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Vadav,N.S.
 TITLE Nucleotide sequences of a new class of diverged delta-9
 steroyl-acp desaturase genes
 JOURNAL Patent: WO 0216565-A 15 28-FEB-2002;
 E. I. du Pont de Nemours and Company (US)
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      375  ArgLeuGlnGluArgAlaAspGluArgAlaGlyIyrMetIyrHisIleGlyValIyr 394
      1101  CGGCGCGCGCGCGCGCTGAGACAGCGCTGAAGAG--GATGAGCAGAGAGAGTCAAG 1157
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LOCUS   Simmondsia chinensis stearoyl-acyl carrier protein desaturase mRNA,
DEFINITION complete cds.
ACCESSION M83199.1 GI:169894
VERSION   M83199.1 GI:169894
KEYWORDS  stearoyl-acyl carrier protein desaturase.
SOURCE    Simmondsia chinensis embryo immature seed cDNA to mRNA.
ORGANISM  Simmondsia chinensis
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          1 (bases 1 to 1576)
REFERENCE  Sato,A., Becker,C.K. and Knauf,V.C.
          Nucleotide sequence of a complementary DNA clone encoding
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          Plant Physiol. 99, 362-363 (1992)
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      647  CTTTAAACAAGATATCTTAACTTACTGTGCTGACATGATGACATAGACATAGACAGACA 706
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DEFINITION desaturase precursor mRNA, complete cds.
ACCESSION U07605
VERSION U07605.1 GI:533085
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ORGANISM Thumbergia alata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Acanthaceae; Thumbergia.
REFERENCE 1 (bases 1 to 1443)
AUTHORS Cahoon,E.B., Becker,C.K., Shanklin,J. and Ohlrogge,J.B.
TITLE cDNAs for isoforms of the delta 9-stearoyl-acyl carrier protein
JOURNAL desaturase from Thumbergia alata endosperm
MEDLINE Plant Physiol. 106 (2), 807-808 (1994)
PUBMED 95083771
7991701
REFERENCE 2 (bases 1 to 1443)
AUTHORS Cahoon,E.B.
TITLE Direct Submission
JOURNAL submitted (08-MAR-1994) Cahoon E. B., Brookhaven National
Laboratory, Biology, Upton, NY 11973, USA
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 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 2243)
 AUTHORS Hitez,W.D., Yadau,N.S., and Perez-Grau,L.
 TITLE Nucleotide sequence of soybean stearyl-ACP desaturase gene
 JOURNAL Patent: US 5443974-A 1 22-AUG-1995;
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 VERSION M59857.1 GI:169716
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 REFERENCE 1 (bases 1 to 1643)
 AUTHORS Shanklin,J. and Somerville,C.
 TITLE Stearyl-acyl-carrier-protein desaturase from higher plants is structurally unrelated to the animal and fungal homologs
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (6), 2510-2514 (1991)
 MEDLINE 91172837

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